

#4

SEQUENCE LISTING

<110> KYOWA HAKKO KOGYO CO., LTD

<120> Novel Transaldolase

<130> 00005.001198

<140> US/10/088,594

<141> 2002-03-21

<150> JP 99/266548

<151> 1999-09-21

<160> 3

<170> PatentIn Ver. 2.0

<210> 1

<211> 1080

<212> DNA

<213> Corynebacterium glutamicum ATCC31388

<400> 1

atg tct cac att gat gat ctt gca cag ctc ggc act tcc act tgg ctc	48
Met Ser His Ile Asp Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu	
1 5 10 15	
gac gac ctc tcc cgc gag cgc att act tcc ggc aat ctc agc cag gtt	96
Asp Asp Leu Ser Arg Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val	
20 25 30	
att gag gaa aag tct gta gtc ggt gtc acc acc aac cca gct att ttc	144
Ile Glu Glu Lys Ser Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe	
35 40 45	
gca gca gca atg tcc aag ggc gat tcc tac gac gct cag atc gca gag	192
Ala Ala Ala Met Ser Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu	
50 55 60	
ctc aag gcc gct ggc gca tct gtt gac cag gct gtt tac gcc atg agc	240
Leu Lys Ala Ala Gly Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser	
65 70 75 80	
atc gac gat gtt cgc aat gct tgt gat ctg ttc acc ggc atc ttc gag	288
Ile Asp Asp Val Arg Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu	
85 90 95	

290

295

300

ggt gac acc ctg tcc aac tcc gcg gca gaa gct gac gct gtg ttc tcc 960
 Gly Asp Thr Leu Ser Asn Ser Ala Ala Glu Ala Asp Ala Val Phe Ser
 305 310 315 320

cag ctt gag gct ctg ggc gtt gac ttg gca gat gtc ttc cag gtc ctg 1008
 Gln Leu Glu Ala Leu Gly Val Asp Leu Ala Asp Val Phe Gln Val Leu
 325 330 335

gag acc gag ggt gtg gac aag ttt gtt gct tct tgg agc gaa ctg ctt 1056
 Glu Thr Glu Gly Val Asp Lys Phe Val Ala Ser Trp Ser Glu Leu Leu
 340 345 350

gag tcc atg gaa gct cgc ctg aag
 Glu Ser Met Glu Ala Arg Leu Lys
 355 360

<210> 2

<211> 1080

<212> DNA

<213> *Corynebacterium glutamicum* ATCC31388

<400> 2

atgtctcaca ttgatgatct tgcacagctc ggcacttcca cttggctcga cgacctctcc 60
 cgcgagcgca ttacttccgg caatctcagc caggttattg aggaaaagtc tgtagtcggt 120
 gtcaccacca acccagctat tttcgcagca gcaatgtcca agggcgattc ctacgacgct 180
 cagatcgag agctcaaggc cgctggcgca tctgttgacc aggctgttta cgccatgagc 240
 atcgacgatg ttcgcaatgc ttgtgatctg ttcaccggca tcttcgagtc ctccaacggc 300
 tacgacggcc gcgtgtccat cgagggtgac ccacgtatct ctgctgaccg cgacgcaacc 360
 ctggctcagg ccaaggagct gtgggcaaag gttgatcgtc caaacgtcat gatcaagatc 420
 cctgcaaccc caggttcttt gccagcaatc accgacgctt tggctgaggg catcagcggt 480
 aacgtcacct tgatcttctc cgttgctcgc taccgcgagg tcatcgctgc gtacatcgag 540
 ggaatcaagc aggcagctgc aaacggccac gacgtatcca agatccactc tgtggcttcc 600
 ttcttcgtct cccgcgtcga cgttgagatc gacaagcgcc tcgaggcaat cggatccgat 660
 gaggctttgg ctctgcgcgg caaggcaggc gttgccaacg ctcagcgcgc ttacgctgtg 720
 tacaaggagc ttttcgacgc cgccgagctg cctgaagggtg ccaacactca gcgcccactg 780

tgggcatcca ccggcgtgaa gaaccctgcg tacgctgcaa ctcttttacgt ttccgagctg 840
 gctgggtccaa acaccgtcaa caccatgccaa gaaggcacca tcgacgctgt tctggaactg 900
 ggcaacctgc acggtgacac cctgtccaac tccgcggcag aagctgacgc tgtgtttctcc 960
 cagcttgagg ctctgggcgt tgacttggca gatgtcttcc aggtcctgga gaccgagggt 1020
 gtggacaagt ttgttgcttc ttggagcgaa ctgcttgagt ccatggaagc tcgcctgaag 1080

<210> 3
 <211> 4108
 <212> DNA
 <213> *Corynebacterium glutamicum* ATCC31388

<221> CDS
 <222> (373)..(2472)

<221> CDS
 <222> (2643)..(3722)

<400> 3
 tcgagagttt gaaggggtcc gattcgttcc gttcgtgacg ctttgtgagg ttttttgacg 60
 ttgcaccgta ttgcttgccg aacatttttc ttttcctttc ggtttttcga gaattttcac 120
 ctacaaaagc ccacgtcaca gctcccagac ttaagattgg tcacaccttt gacacatttg 180
 aaccacagtt gggtataaaa tgggttcaac atcactatgg ttagagggtgt tgacgggtca 240
 gattaagcaa agactacttt cggggtagat cacctttgcc aaatttgaat caattaacct 300
 aagtcgtaga tctgatcatc ggatctaacg aaaacgaacc aaaacttttg tcccgggtta 360
 acccaggaag ga atg acc acc ttg acg ctg tca cct gaa ctt cag gcg ctc 411
 Met Thr Thr Leu Thr Leu Ser Pro Glu Leu Gln Ala Leu
 1 5 10

act gta cgc aat tac ccc tct gat tgg tcc gat gtg gac acc aag gct 459
 Thr Val Arg Asn Tyr Pro Ser Asp Trp Ser Asp Val Asp Thr Lys Ala
 15 20 25

gta gac act gtt cgt gtc ctc gct gca gac gct gta gaa aac tgt ggc 507
 Val Asp Thr Val Arg Val Leu Ala Ala Asp Ala Val Glu Asn Cys Gly
 30 35 40 45

tcc ggc cac cca ggc acc gca atg agc ctg gct ccc ctt gca tac acc 555
 Ser Gly His Pro Gly Thr Ala Met Ser Leu Ala Pro Leu Ala Tyr Thr
 50 55 60

ttg tac cag cgg gtt atg aac gta gat cca cag gac acc aac tgg gca	603
Leu Tyr Gln Arg Val Met Asn Val Asp Pro Gln Asp Thr Asn Trp Ala	
65 70 75	
ggc cgt gac cgc ttc gtt ctt tct tgt ggc cac tcc tct ttg acc cag	651
Gly Arg Asp Arg Phe Val Leu Ser Cys Gly His Ser Ser Leu Thr Gln	
80 85 90	
tac atc cag ctt tac ttg ggt gga ttc ggc ctt gag atg gat gac ctg	699
Tyr Ile Gln Leu Tyr Leu Gly Gly Phe Gly Leu Glu Met Asp Asp Leu	
95 100 105	
aag gct ctg cgc acc tgg gat tcc ttg acc cca gga cac cct gag tac	747
Lys Ala Leu Arg Thr Trp Asp Ser Leu Thr Pro Gly His Pro Glu Tyr	
110 115 120 125	
cgc cac acc aag ggc gtt gag atc acc act ggc cct ctt ggc cag ggt	795
Arg His Thr Lys Gly Val Glu Ile Thr Thr Gly Pro Leu Gly Gln Gly	
130 135 140	
ctt gca tct gca gtt ggt atg gcc atg gct gct cgt cgt gag cgt ggc	843
Leu Ala Ser Ala Val Gly Met Ala Met Ala Ala Arg Arg Glu Arg Gly	
145 150 155	
cta ttc gac cca acc gct gct gag ggc gaa tcc cca ttc gac cac cac	891
Leu Phe Asp Pro Thr Ala Ala Glu Gly Glu Ser Pro Phe Asp His His	
160 165 170	
atc tac gtc att gct tct gat ggt gac ctg cag gaa ggt gtc acc tct	939
Ile Tyr Val Ile Ala Ser Asp Gly Asp Leu Gln Glu Gly Val Thr Ser	
175 180 185	
gag gca tcc tcc atc gct ggc acc cag cag ctg ggc aac ctc atc gtg	987
Glu Ala Ser Ser Ile Ala Gly Thr Gln Gln Leu Gly Asn Leu Ile Val	
190 195 200 205	
ttc tgg gat gac aac cgc atc tcc atc gaa gac aac act gag atc gct	1035
Phe Trp Asp Asp Asn Arg Ile Ser Ile Glu Asp Asn Thr Glu Ile Ala	
210 215 220	
ttc aac gag gac gtt gtt gct cgt tac aag gct tac ggc tgg cag acc	1083
Phe Asn Glu Asp Val Val Ala Arg Tyr Lys Ala Tyr Gly Trp Gln Thr	
225 230 235	
att gag gtt gag gct ggc gag gac gtt gca gca atc gaa gct gca gtg	1131
Ile Glu Val Glu Ala Gly Glu Asp Val Ala Ala Ile Glu Ala Ala Val	
240 245 250	
gct gag gct aag aag gac acc aag cga cct acc ttc atc cgc gtt cgc	1179
Ala Glu Ala Lys Lys Asp Thr Lys Arg Pro Thr Phe Ile Arg Val Arg	

255					260					265						
acc	atc	atc	ggc	ttc	cca	gct	cca	acc	atg	atg	aac	acc	ggt	gct	gtg	1227
Thr	Ile	Ile	Gly	Phe	Pro	Ala	Pro	Thr	Met	Met	Asn	Thr	Gly	Ala	Val	
270					275				280						285	
cac	ggt	gct	gct	ctt	ggc	gca	gct	gag	ggt	gca	gca	acc	aag	act	gag	1275
His	Gly	Ala	Ala	Leu	Gly	Ala	Ala	Glu	Val	Ala	Ala	Thr	Lys	Thr	Glu	
				290				295						300		
ctt	gga	ttc	gat	cct	gag	gct	cac	ttc	gcg	atc	gac	gat	gag	ggt	atc	1323
Leu	Gly	Phe	Asp	Pro	Glu	Ala	His	Phe	Ala	Ile	Asp	Asp	Glu	Val	Ile	
			305					310					315			
gct	cac	acc	cgc	tcc	ctc	gca	gag	cgc	gct	gca	cag	aag	aag	gct	gca	1371
Ala	His	Thr	Arg	Ser	Leu	Ala	Glu	Arg	Ala	Ala	Gln	Lys	Lys	Ala	Ala	
		320					325					330				
tgg	cag	gtc	aag	ttc	gat	gag	tgg	gca	gct	gcc	aac	cct	gag	aac	aag	1419
Trp	Gln	Val	Lys	Phe	Asp	Glu	Trp	Ala	Ala	Ala	Asn	Pro	Glu	Asn	Lys	
	335					340					345					
gct	ctg	ttc	gat	cgc	ctg	aac	tcc	cgt	gag	ctt	cca	gcg	ggc	tac	gct	1467
Ala	Leu	Phe	Asp	Arg	Leu	Asn	Ser	Arg	Glu	Leu	Pro	Ala	Gly	Tyr	Ala	
350					355					360					365	
gac	gag	ctc	cca	aca	tgg	gat	gca	gat	gag	aag	ggc	gtc	gca	act	cgt	1515
Asp	Glu	Leu	Pro	Thr	Trp	Asp	Ala	Asp	Glu	Lys	Gly	Val	Ala	Thr	Arg	
				370					375					380		
aag	gct	tcc	gag	gct	gca	ctt	cag	gca	ctg	ggc	aag	acc	ctt	cct	gag	1563
Lys	Ala	Ser	Glu	Ala	Ala	Leu	Gln	Ala	Leu	Gly	Lys	Thr	Leu	Pro	Glu	
			385					390					395			
ctg	tgg	ggc	ggt	tcc	gct	gac	ctc	gca	ggt	tcc	aac	aac	acc	gtg	atc	1611
Leu	Trp	Gly	Gly	Ser	Ala	Asp	Leu	Ala	Gly	Ser	Asn	Asn	Thr	Val	Ile	
		400					405					410				
aag	ggc	tcc	cct	tcc	ttc	ggc	cct	gag	tcc	atc	tcc	acc	gag	acc	tgg	1659
Lys	Gly	Ser	Pro	Ser	Phe	Gly	Pro	Glu	Ser	Ile	Ser	Thr	Glu	Thr	Trp	
	415					420					425					
tct	gct	gag	cct	tac	ggc	cgt	aac	ctg	cac	ttc	ggt	atc	cgt	gag	cac	1707
Ser	Ala	Glu	Pro	Tyr	Gly	Arg	Asn	Leu	His	Phe	Gly	Ile	Arg	Glu	His	
430					435					440					445	
gct	atg	gga	tcc	atc	ctc	aac	ggc	att	tcc	ctc	cac	ggt	ggc	acc	cgc	1755
Ala	Met	Gly	Ser	Ile	Leu	Asn	Gly	Ile	Ser	Leu	His	Gly	Gly	Thr	Arg	
				450				455						460		

cca	tac	ggt	gga	acc	ttc	ctc	atc	ttc	tcc	gac	tac	atg	cgt	cct	gca	1803
Pro	Tyr	Gly	Gly	Thr	Phe	Leu	Ile	Phe	Ser	Asp	Tyr	Met	Arg	Pro	Ala	
			465					470					475			
gtt	cgt	ctt	gca	gct	ctc	atg	gag	acc	gac	gct	tac	tac	gtc	tgg	acc	1851
Val	Arg	Leu	Ala	Ala	Leu	Met	Glu	Thr	Asp	Ala	Tyr	Tyr	Val	Trp	Thr	
		480					485					490				
cac	gac	tcc	atc	ggt	ctg	ggc	gaa	gat	ggc	cca	acc	cac	cag	cct	gtt	1899
His	Asp	Ser	Ile	Gly	Leu	Gly	Glu	Asp	Gly	Pro	Thr	His	Gln	Pro	Val	
	495					500					505					
gaa	acc	ttg	gct	gcg	ctg	cgc	gcc	atc	cca	ggt	ctg	tcc	gtc	ctg	cgt	1947
Glu	Thr	Leu	Ala	Ala	Leu	Arg	Ala	Ile	Pro	Gly	Leu	Ser	Val	Leu	Arg	
510					515					520					525	
cct	gca	gat	gcg	aat	gag	acc	gcc	cag	gct	tgg	gct	gca	gca	ctt	gag	1995
Pro	Ala	Asp	Ala	Asn	Glu	Thr	Ala	Gln	Ala	Trp	Ala	Ala	Ala	Leu	Glu	
				530					535					540		
tac	aag	gaa	ggc	cct	aag	ggt	ctt	gca	ctg	acc	cgc	cag	aac	gtt	cct	2043
Tyr	Lys	Glu	Gly	Pro	Lys	Gly	Leu	Ala	Leu	Thr	Arg	Gln	Asn	Val	Pro	
			545					550					555			
gtt	ctg	gaa	ggc	acc	aag	gag	aag	gct	gct	gaa	ggc	gtt	cgc	cgc	ggt	2091
Val	Leu	Glu	Gly	Thr	Lys	Glu	Lys	Ala	Ala	Glu	Gly	Val	Arg	Arg	Gly	
		560					565					570				
ggc	tac	gtc	ctg	gtt	gag	ggt	tcc	aag	gaa	acc	cca	gat	gtg	atc	ctc	2139
Gly	Tyr	Val	Leu	Val	Glu	Gly	Ser	Lys	Glu	Thr	Pro	Asp	Val	Ile	Leu	
	575					580					585					
atg	ggc	tcc	ggc	tcc	gag	gtt	cag	ctt	gca	gtt	aac	gct	gcg	aaa	gct	2187
Met	Gly	Ser	Gly	Ser	Glu	Val	Gln	Leu	Ala	Val	Asn	Ala	Ala	Lys	Ala	
590					595					600					605	
ctg	gaa	gct	gag	ggc	gtt	gca	gct	cgc	gtt	gtt	tca	gtt	cct	tgc	atg	2235
Leu	Glu	Ala	Glu	Gly	Val	Ala	Ala	Arg	Val	Val	Ser	Val	Pro	Cys	Met	
				610					615					620		
gat	tgg	ttc	cag	gag	cag	gac	gca	gag	tac	atc	gag	tcc	gtt	ctg	cct	2283
Asp	Trp	Phe	Gln	Glu	Gln	Asp	Ala	Glu	Tyr	Ile	Glu	Ser	Val	Leu	Pro	
			625					630					635			
gca	gct	gtg	acc	gct	cgt	gtg	tct	gtt	gaa	gct	ggc	atc	gca	atg	cct	2331
Ala	Ala	Val	Thr	Ala	Arg	Val	Ser	Val	Glu	Ala	Gly	Ile	Ala	Met	Pro	
		640					645					650				
tgg	tac	cgc	ttc	ttg	ggc	acc	cag	ggc	cgt	gct	gtc	tcc	ctt	gag	cac	2379
Trp	Tyr	Arg	Phe	Leu	Gly	Thr	Gln	Gly	Arg	Ala	Val	Ser	Leu	Glu	His	

/

655	660	665	
ttc ggt gct tct gcg gat tac cag acc ctg ttt gag aag ttc ggc atc			2427
Phe Gly Ala Ser Ala Asp Tyr Gln Thr Leu Phe Glu Lys Phe Gly Ile			
670	675	680	685
acc acc gat gca gtc gtg gca gcg gcc aag gac tcc att aac agt			2472
Thr Thr Asp Ala Val Val Ala Ala Ala Lys Asp Ser Ile Asn Ser			
	690	695	700
taattgccct gctgttttta gcttcaaccc ggggcagtat gattctccgg aattttattg			2532
ccccgggttg ttgttgtaa tcggtacaaa gggctttaag cacatccctt acttgcctgc			2592
tctccttgag cacagttcaa gaacaattct tttaaggaaa atttagtttc atg tct			2648
		Met Ser	
		1	
cac att gat gat ctt gca cag ctc ggc act tcc act tgg ctc gac gac			2696
His Ile Asp Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu Asp Asp			
	5	10	15
ctc tcc cgc gag cgc att act tcc ggc aat ctc agc cag gtt att gag			2744
Leu Ser Arg Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val Ile Glu			
	20	25	30
gaa aag tct gta gtc ggt gtc acc acc aac cca gct att ttc gca gca			2792
Glu Lys Ser Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe Ala Ala			
	35	40	50
gca atg tcc aag ggc gat tcc tac gac gct cag atc gca gag ctc aag			2840
Ala Met Ser Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu Leu Lys			
	55	60	65
gcc gct ggc gca tct gtt gac cag gct gtt tac gcc atg agc atc gac			2888
Ala Ala Gly Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser Ile Asp			
	70	75	80
gat gtt cgc aat gct tgt gat ctg ttc acc ggc atc ttc gag tcc tcc			2936
Asp Val Arg Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu Ser Ser			
	85	90	95
aac ggc tac gac ggc cgc gtg tcc atc gag gtt gac cca cgt atc tct			2984
Asn Gly Tyr Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg Ile Ser			
	100	105	110
gct gac cgc gac gca acc ctg gct cag gcc aag gag ctg tgg gca aag			3032
Ala Asp Arg Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp Ala Lys			
	115	120	130
gtt gat cgt cca aac gtc atg atc aag atc cct gca acc cca ggt tct			3080

Val	Asp	Arg	Pro	Asn	Val	Met	Ile	Lys	Ile	Pro	Ala	Thr	Pro	Gly	Ser		
				135					140					145			
ttg	cca	gca	atc	acc	gac	gct	ttg	gct	gag	ggc	atc	agc	gtt	aac	gtc	3128	
Leu	Pro	Ala	Ile	Thr	Asp	Ala	Leu	Ala	Glu	Gly	Ile	Ser	Val	Asn	Val		
			150					155					160				
acc	ttg	atc	ttc	tcc	gtt	gct	cgc	tac	cgc	gag	gtc	atc	gct	gcg	tac	3176	
Thr	Leu	Ile	Phe	Ser	Val	Ala	Arg	Tyr	Arg	Glu	Val	Ile	Ala	Ala	Tyr		
		165					170					175					
atc	gag	gga	atc	aag	cag	gca	gct	gca	aac	ggc	cac	gac	gta	tcc	aag	3224	
Ile	Glu	Gly	Ile	Lys	Gln	Ala	Ala	Ala	Asn	Gly	His	Asp	Val	Ser	Lys		
	180					185					190						
atc	cac	tct	gtg	gct	tcc	ttc	ttc	gtc	tcc	cgc	gtc	gac	gtt	gag	atc	3272	
Ile	His	Ser	Val	Ala	Ser	Phe	Phe	Val	Ser	Arg	Val	Asp	Val	Glu	Ile		
195					200					205					210		
gac	aag	cgc	ctc	gag	gca	atc	gga	tcc	gat	gag	gct	ttg	gct	ctg	cgc	3320	
Asp	Lys	Arg	Leu	Glu	Ala	Ile	Gly	Ser	Asp	Glu	Ala	Leu	Ala	Leu	Arg		
			215						220					225			
ggc	aag	gca	ggc	gtt	gcc	aac	gct	cag	cgc	gct	tac	gct	gtg	tac	aag	3368	
Gly	Lys	Ala	Gly	Val	Ala	Asn	Ala	Gln	Arg	Ala	Tyr	Ala	Val	Tyr	Lys		
			230					235					240				
gag	ctt	ttc	gac	gcc	gcc	gag	ctg	cct	gaa	ggc	gcc	aac	act	cag	cgc	3416	
Glu	Leu	Phe	Asp	Ala	Ala	Glu	Leu	Pro	Glu	Gly	Ala	Asn	Thr	Gln	Arg		
		245					250					255					
cca	ctg	tgg	gca	tcc	acc	ggc	gtg	aag	aac	cct	gcg	tac	gct	gca	act	3464	
Pro	Leu	Trp	Ala	Ser	Thr	Gly	Val	Lys	Asn	Pro	Ala	Tyr	Ala	Ala	Thr		
	260					265					270						
ctt	tac	gtt	tcc	gag	ctg	gct	ggc	cca	aac	acc	gtc	aac	acc	atg	cca	3512	
Leu	Tyr	Val	Ser	Glu	Leu	Ala	Gly	Pro	Asn	Thr	Val	Asn	Thr	Met	Pro		
275					280					285					290		
gaa	ggc	acc	atc	gac	gct	gtt	ctg	gaa	ctg	ggc	aac	ctg	cac	ggc	gac	3560	
Glu	Gly	Thr	Ile	Asp	Ala	Val	Leu	Glu	Leu	Gly	Asn	Leu	His	Gly	Asp		
				295					300					305			
acc	ctg	tcc	aac	tcc	gcg	gca	gaa	gct	gac	gct	gtg	ttc	tcc	cag	ctt	3608	
Thr	Leu	Ser	Asn	Ser	Ala	Ala	Glu	Ala	Asp	Ala	Val	Phe	Ser	Gln	Leu		
			310					315					320				
gag	gct	ctg	ggc	gtt	gac	ttg	gca	gat	gtc	ttc	cag	gtc	ctg	gag	acc	3656	
Glu	Ala	Leu	Gly	Val	Asp	Leu	Ala	Asp	Val	Phe	Gln	Val	Leu	Glu	Thr		
		325					330					335					

gag ggt gtg gac aag ttt gtt gct tct tgg agc gaa ctg ctt gag tcc 3704
Glu Gly Val Asp Lys Phe Val Ala Ser Trp Ser Glu Leu Leu Glu Ser
340 345 350

atg gaa gct cgc ctg aag tagaatcagc acgctgcatc agtaacggcg 3752
Met Glu Ala Arg Leu Lys
355 360

acatgaaatc gaattagttc gatccttatgt ggccggttaca catcttttcát taaagaaagg 3812

atcgtgacgc taccatcgtg agcacaaaca cgacccccctc cagctgggaca aaccactgc 3872

gcgacccgca ggataaacga ctcccccgca tcgctggccc ttccggcatg gtgatcttcg 3932

gtgtcactgg cgacttggct cgaaggaagc tgctccccgc catttatgat ctagcaaacc 3992

gcggattgct gccccagga ttctcgttgg taggttacgg ccgccgcgaa tggtccaaag 4052

aagactttga aaaatacgta cgcgatgccg caagtgctgg tgctcgtacg gaattc 4108